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*Parcy, F., O. Nilsson,
M.A. Busch, I. Lee, D.
Weigel. A genetic
framework for floral
patterning. Nature
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Cover Stories:

Major Scientific Publications Featuring NRI-funded Research



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How are the parts of a flower made different from each other? This is the question that Weigel and colleagues at the Salk Institute asked in a NRI-funded study. The researchers already knew that the development of individual flowers is initiated by meristem-identity genes that specify that young buds become flowers instead of leaves or shoots. They also knew that the four major types of floral organs (sepals, petals, stamens, and ovaries/carpels) do not develop without the activity of three classes of homeotic genes, which distinguish the different organs from each other and are active only in flowers. One homeotic class is needed for sepals and petals, a second class for petals and stamens, and a third for stamens and carpels. In the absence of any homeotic gene, all floral organs are replaced by leaves. Because meristem-identity genes become active before homeotic genes, the meristem-identity genes are likely to be involved in the activation of the homeotic genes. In this research, Weigel and colleagues showed that meristem-identity genes can activate homeotic genes independently of floral development. Hence, activation of homeotic genes is not an automatic consequence of established floral fate. They also showed that the mechanisms behind the activation of each of the three homeotic gene classes by the meristem-identity genes appear to be different and separate. Understanding the detailed mechanisms behind flower development and the development of individual organs within a flower could lead to more sophisticated manipulation and control of agricultural plant breeding systems.

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